cccAAGCTTGCTAGAAATATGAACCTTCC-3' (SEQ ID NO: 12) are used to amplify *RHO1* coding sequence with 1 kilobase of upstream regulatory sequence and 500 basepairs of downstream regulatory sequence. *Bam*HI and *Hind*III restriction sites are added to the oligonucleotides to facilitate cloning into the pRS416 centromere-based yeast vector. The Quik Change Site-Directed Mutagenesis Kit (Stratagene, La Jolla CA) is used to first create a mutation that encodes the G22S substitution; next, the pRS416*rho1G22S* plasmid is used as a template to introduce a mutation that encodes the D125N substitution. Primer pair 5'-gtgcctgtAgtaagacatgt-3' (SEQ ID NO: 441)/ 5'-acatgtcttacTacaggcac-3'(SEQ ID NO: 442) is used to anneal to the pRS416*RHO1* template for pRS416*rho1G22S* allele construction. Primer pair 5'-gtaaagtgAatttgagaaac-3' (SEQ ID NO: 443)/ 5'- gtttctcaaatTcactttac-3' (SEQ ID NO: 444) is used to anneal to the pRS416*rho1G22S* template for pRS416*rho1G22S D125N* allele construction. pRS416*rho1G22S D125N* and control plasmids (pRS416*RHO1* and pRS416) are then used to transform a wild-type *ura3* auxotrophic strain. Transformants are selected and grown at 25°C in synthetic liquid growth medium lacking uracil and containing the osmolyte sorbitol (1M). Cultures are then transferred to growth in synthetic liquid growth medium lacking uracil without sorbitol, and cells are visually inspected following growth for various periods of time. Expression of the *rho1G22S D125N* dominant allele causes cell lysis after growth for approximately 120 minutes.--

Replace the paragraph beginning at page 78, line 28 with the following rewritten paragraph:

-- *RSR1* coding sequence for construction of dominant mutations can be isolated from *Saccharomyces cerevisiae* genomic DNA. Primers 5'-cgc**GGATCC**TATCTTCACTCAATATACTTCCTA-3' (SEQ ID NO: 17) and 5'-ccc**AAGCTT**CATCGTTGAAACTTGATAACGCAC-3' (SEQ ID NO: 18) are used to amplify *RHO1* coding sequence with 750 basepairs of upstream regulatory sequence and 500 basepairs of downstream regulatory sequence. *Bam*HI and *Hind*III restriction sites are added to the oligonucleotides to facilitate cloning into the pRS416 centromere-based yeast vector. The Quik Change Site-Directed Mutagenesis Kit (Stratagene, La Jolla CA) is used to create dominant-

negative *RSR1* substitution mutation K16N. Primer pair 5'- tggtgtcggtaa**T**tcctgcttaac-3' (SEQ ID NO: 445) / 5'- gttaagcagga**A**ttaccgacacca-3' (SEQ ID NO: 446) is used to anneal to the pRS416*RSR1* template for allele construction. The pRS416*rsr1K16N* and control pRS416 plasmids are then used to transform a haploid wild-type *ura3* auxotrophic strain. Transformants are selected and grown at 30°C in YPD liquid growth medium. Log phase cultures are fixed in 3.7% formaldehyde (vol:vol) and stained with the chitin-binding dye Calcofluor white, as described; previous sites of bud formation are marked with a chitin-rich structure called a bud scar. Fluorescent microscopy reveals that cells containing the control plasmid display clustering of bud scars at one pole of the cells, the well-characterized haploid pattern of bud site selection. Cells expressing *rsr1K16N* display a random pattern of bud site selection; bud scars are scattered across the surface of haploid cells. Cells expressing *rsr1K16N* do not display other obvious growth or morphological defects.--

Please amend the Table 1 page 1 line 3 to reed as:

-- **Gene** **SEQ ID NOs: 21-440 respectively** **Organisms**--